

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/528,684
Source: PTO
Date Processed by STIC: 1/31/06

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/528,684

DATE: 01/31/2006

TIME: 16:15:04

Input Set : A:\211010031U3.txt
 Output Set: N:\CRF4\01312006\J528684.raw

4 <110> APPLICANT: Fleckenstein, Annette E.
 5 Hanson, Glen R.
 7 <120> TITLE OF INVENTION: MODULATING VESICULAR MONOAMINE TRANSPORTER
 8 TRAFFICKING AND FUNCTION: A NOVEL APPROACH FOR
 9 THE TREATMENT OF PARKINSON'S DISEASE
 11 <130> FILE REFERENCE: 21101.0031U3
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,684
 C--> 13 <141> CURRENT FILING DATE: 2005-03-21
 13 <150> PRIOR APPLICATION NUMBER: PCT/US03/29668
 14 <151> PRIOR FILING DATE: 2003-09-19
 16 <150> PRIOR APPLICATION NUMBER: 60/412,439
 17 <151> PRIOR FILING DATE: 2002-09-19
 19 <160> NUMBER OF SEQ ID NOS: 18
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 515
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 30 synthetic construct
 32 <400> SEQUENCE: 1
 33 Met Ala Leu Ser Asp Leu Val Leu Leu Arg Trp Leu Arg Asp Ser Arg
 34 1 5 10 15
 35 His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
 36 20 25 30
 37 Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
 38 35 40 45
 39 Tyr Ser Ile Lys His Glu Lys Asn Ser Thr Glu Ile Gln Thr Thr Arg
 40 50 55 60
 41 Pro Glu Leu Val Val Ser Thr Ser Glu Ser Ile Phe Ser Tyr Tyr Asn
 42 65 70 75 80
 43 Asn Ser Thr Val Leu Ile Thr Gly Asn Ala Thr Gly Thr Leu Pro Gly
 44 85 90 95
 45 Gly Gln Ser His Lys Ala Thr Ser Thr Gln His Thr Val Ala Asn Thr
 46 100 105 110
 47 Thr Val Pro Ser Asp Cys Pro Ser Glu Asp Arg Asp Leu Leu Asn Glu
 48 115 120 125
 49 Asn Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu
 50 130 135 140
 51 Leu Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro
 52 145 150 155 160
 53 Ile Pro Met Phe Ala Gly Phe Cys Ile Met Phe Ile Ser Thr Val Met

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54 165 170 175
 55 Phe Ala Phe Ser Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu
 56 180 185 190
 57 Gln Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu
 58 195 200 205
 59 Ala Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Ala Met Gly Ile
 60 210 215 220
 61 Ala Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly
 62 225 230 235 240
 63 Ser Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu
 64 245 250 255
 65 Ala Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln
 66 260 265 270
 67 Pro Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr
 68 275 280 285
 69 Leu Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe
 70 290 295 300
 71 Ala Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met
 72 305 310 315 320
 73 Met Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu
 74 325 330 335
 75 Pro Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu
 76 340 345 350
 77 Ala His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Val Ile
 78 355 360 365
 79 Val Gly Ile Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly
 80 370 375 380
 81 Leu Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp
 82 385 390 395 400
 83 Ser Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val
 84 405 410 415
 85 Ser Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met
 86 420 425 430
 87 Gly Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile
 88 435 440 445
 89 Gly Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Ala Phe
 90 450 455 460
 91 Ala Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys
 92 465 470 475 480
 93 Met Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr
 94 485 490 495
 95 Thr Gln Asn Asn Val Gln Ser Tyr Pro Ile Gly Asp Asp Glu Glu Ser
 96 500 505 510
 97 Glu Ser Asp
 98 515
 100 <210> SEQ ID NO: 2
 101 <211> LENGTH: 1548
 102 <212> TYPE: DNA
 103 <213> ORGANISM: Artificial Sequence

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105 <220> FEATURE:

106 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
107 synthetic construct

109 <400> SEQUENCE: 2

110	atggccctga	gcgatctgg	gtctgcgaga	tggctgcggg	acagccgcca	ctcgcgcaaa	60
111	ctgatcctgt	tcatcggtt	ccttgcgtg	ctgtggaca	acatgtgt	caccgtcg	120
112	gttccatca	tcccagcta	tctgtacagc	attaagcatg	agaaaaactc	tacggaaatc	180
113	cagaccacca	gaccagagct	cgtggcttcc	acctccgaaa	gcatcttctc	ttactataac	240
114	aactctactg	tgttgcac	cggaaatgcc	actgggactc	ttccaggagg	gca	300
115	aaggctacca	gcacacagca	cactgtgg	aacaccactg	tcccttcg	ctgtcccagt	360
116	gaagacagag	accttctgaa	tgagaatgtg	caagttggc	tgctgttgc	ctccaaagcc	420
117	actgtccagc	tcctcactaa	cccattcata	ggacttctg	ccaacagaat	tggctatcca	480
118	attccatgt	ttgcggctt	ctgcacat	tttatctcaa	cagttatgtt	tgcccttctcc	540
119	agcagctatg	ccttctgt	gatgccagg	tcccttcagg	gaattggc	ctctgtca	600
120	tccgtggctg	ggatgggtat	gctggccagc	gtgtacacag	atgatgagga	gagggggaa	660
121	gcccattggca	ttgcgttggg	tggcctggcc	atgggagtct	tagtggacc	ccccttcggg	720
122	agtgtgtct	atgagttgt	ggggaaagaca	gctccctcc	tggtgctagc	tgcccttgg	780
123	ctcttggatg	gggctattca	gctcttgc	ctccagccgt	cccagatc	gccagagagt	840
124	cagaagggga	cacccatca	gaccttgc	aaggatccat	acatccat	cgctgcaggc	900
125	tccatctgt	ttgcaaacat	ggggatagcc	atgcggc	ccgcccgtcc	catctggatg	960
126	atggagacca	tgttccc	aaagtggcag	ctggcgtt	cttcctccc	ggcagacatc	1020
127	tcttatctca	ttgaaaccaa	tattttgg	atacttgcac	acaaaatgg	aagtggcta	1080
128	tgtgtcttc	ttggaaatgg	aattgttgg	atcagcat	tatgcatccc	cttgc	1140
129	aatatctatg	gactcatcgc	tcccaactt	ggagttgg	ttgcaatgg	gatggggac	1200
130	tcctctatga	tgcctatcat	gggctaccc	gttgcac	ggcatgtgc	tgtctatgg	1260
131	agtgtttatg	ccattgcaga	cgtggcctt	tgtatgg	atgctatcg	tccctctg	1320
132	gggtggc	tcgcaaaaggc	aattggctt	ccttggctt	tgacaattat	tggataatt	1380
133	gatatcgctt	ttgccttact	ctgttttcc	cttgcagtc	cacctgtcaa	ggaggaaaa	1440
134	atggctatcc	tcatggacca	caactgtccc	attaaaacaa	agatgtacac	tcagaataat	1500
135	gtccagtcat	atccatcg	tgatgatgaa	gaatctgaaa	gtgactg		1548

137 <210> SEQ ID NO: 3

138 <211> LENGTH: 514

139 <212> TYPE: PRT

140 <213> ORGANISM: Artificial Sequence

142 <220> FEATURE:

143 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =

144 synthetic construct

146 <400> SEQUENCE: 3

147	Met	Ala	Leu	Ser	Glu	Leu	Ala	Leu	Val	Arg	Trp	Leu	Gln	Glu	Ser	Arg
148	1				5				10				15			
149	His	Ser	Arg	Lys	Leu	Ile	Leu	Phe	Ile	Val	Phe	Leu	Ala	Leu	Leu	
150					20				25				30			
151	Asp	Asn	Met	Leu	Leu	Thr	Val	Val	Val	Pro	Ile	Ile	Pro	Ser	Tyr	Leu
152					35				40				45			
153	Tyr	Ser	Ile	Lys	His	Glu	Lys	Asn	Ala	Thr	Glu	Ile	Gln	Thr	Ala	Arg
154					50				55				60			
155	Pro	Val	His	Thr	Ala	Ser	Ile	Ser	Asp	Ser	Phe	Gln	Ser	Ile	Phe	Ser
156					65				70				75			80
157	Tyr	Tyr	Asp	Asn	Ser	Thr	Met	Val	Thr	Gly	Asn	Ala	Thr	Arg	Asp	Leu

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158	85	90	95	
159	Thr Leu His Gln Thr Ala Thr Gln His Met Val Thr Asn Ala Ser Ala			
160	100	105	110	
161	Val Pro Ser Asp Cys Pro Ser Glu Asp Lys Asp Leu Leu Asn Glu Asn			
162	115	120	125	
163	Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu Ile			
164	130	135	140	
165	Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro Ile			
166	145	150	155	160
167	Pro Ile Phe Ala Gly Phe Cys Ile Met Phe Val Ser Thr Ile Met Phe			
168	165	170	175	
169	Ala Phe Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu Gln			
170	180	185	190	
171	Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu Ala			
172	195	200	205	
173	Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Val Met Gly Ile Ala			
174	210	215	220	
175	Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly Ser			
176	225	230	235	240
177	Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu Ala			
178	245	250	255	
179	Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln Pro			
180	260	265	270	
181	Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr Leu			
182	275	280	285	
183	Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe Ala			
184	290	295	300	
185	Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met Met			
186	305	310	315	320
187	Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu Pro			
188	325	330	335	
189	Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu Ala			
190	340	345	350	
191	His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Ile Ile Val			
192	355	360	365	
193	Gly Val Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly Leu			
194	370	375	380	
195	Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp Ser			
196	385	390	395	400
197	Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val Ser			
198	405	410	415	
199	Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met Gly			
200	420	425	430	
201	Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile Gly			
202	435	440	445	
203	Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Leu Phe Ala			
204	450	455	460	
205	Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys Met			
206	465	470	475	480

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207 Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr Thr
 208 485 490 495
 209 Gln Asn Asn Ile Gln Ser Tyr Pro Ile Gly Glu Asp Glu Glu Ser Glu
 210 500 505 510
 211 Ser Asp
 214 <210> SEQ ID NO: 4
 215 <211> LENGTH: 1545
 216 <212> TYPE: DNA
 217 <213> ORGANISM: Artificial Sequence
 219 <220> FEATURE:
 220 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 221 synthetic construct
 223 <400> SEQUENCE: 4
 224 atggccctga gcgagctggc gctggtccgc tggctgcagg agagccgcca ctcgcggaag 60
 225 ctcatcctgt tcatcgtgtt cctggcgctg ctgctggaca acatgctgct cactgtcgtg 120
 226 gtccccatca tcccaagttt tctgtacagc attaagcatg agaagaatgc tacagaaatc 180
 227 cagacggcca ggccagtgc aactgcctcc atctcagaca gcttccagag catcttctcc 240
 228 tattatgata actcgactat ggtcaccggg aatgtacca gagacctgac acttcatcag 300
 229 accgccacac agcacatggt gaccaacgcg tccgctgtt cttccgactg tcccagtgaa 360
 230 gacaaaagacc tcctgaatga aaacgtgcaaa gttggctgtt tgtttgcctc gaaagccacc 420
 231 gtccagctca tcaccaaccc tttcatagga ctactgacca acagaattgg ctatccaatt 480
 232 cccatatttgc cgggattctg catcatgtt gtctcaacaa ttatgtttgc cttctccagc 540
 233 agctatgcct tcctgctgat tgccaggtcg ctgcaggcga tcggctcgat ctgctccctc 600
 234 gtggctggga tgggcatgct tgccagtgtc tacacagatg atgaagagag aggcaacgtc 660
 235 atggaaatcg ctttgggagg cctggccatg ggggtcttag tggggccccc cttcgggaggt 720
 236 gtgctctatg agtttgggg gaagacggct ccgttcctgg tgctggccgc cctggtaactc 780
 237 ttggatggag ctattcagct ctttgcgtc cagccgtccc ggggtgcagcc agagagtca 840
 238 aaggggacac ccctaaccac gctgctgaag gacccgtaca tcctcattgc tgcaaggctcc 900
 239 atctgcttttgc caaacatggg catgcccattt ctggagccat ccctgcccattt ctggatgatg 960
 240 gagaccatgt gttcccgaaa gttcccgatgtt ggcgttcgtt tcttgcctc tagtatctct 1020
 241 tatctcatttgc gaaccaatattttttggata cttgcacaca aaatggggag gtggctttgt 1080
 242 gctttctgg gaatgataat tttttggatgtt agcattttat gtattccatt tgcaaaaaaaac 1140
 243 atttatggac tcatacgatcc gaaactttggatgtt gttggatgtt caattggaaat gttggattcg 1200
 244 tcaatgatgc ctatcatggg ctacatcgatcc gacctgcggc acgtgtccgt ctatggagat 1260
 245 gtgtacgcca ttgcggatgtt ggcattttgtt atggggatgtt ctataggatcc ttctgctgg 1320
 246 ggtgttatttgc caaaggcaat tggatgttcca tggctcatgatca caatttattgg gataattgtat 1380
 247 attcttttgc cccctctctg ctttttctt cgaagtccac ctgccaaggaa agaaaaaaatg 1440
 248 gctattctca tggatcacaat ctgccttatttgc caaaggcaat tggatgttcca tggctcatgatca gaataatatc 1500
 249 cagtcataatc cgataggatgc agatgaagaa tctgaaatgtt actgtt
 251 <210> SEQ ID NO: 5
 252 <211> LENGTH: 525
 253 <212> TYPE: PRT
 254 <213> ORGANISM: Artificial Sequence
 256 <220> FEATURE:
 257 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 258 synthetic construct
 260 <400> SEQUENCE: 5
 261 Met Leu Arg Thr Ile Leu Asp Ala Pro Gln Arg Leu Leu Lys Glu Gly
 262 1 5 10 15

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date